AMENDMENTS

In the Specification:

Please amend the paragraph beginning on Page 16, line 11, as follows:

The NCBI Basic Local Alignment Search Tool (BLAST) (Altschul *et al.*, 1990) is available from several sources including the National Center for Biotechnology Information (NCBI, Bethesda, MD) and on the Internet, for use in connection with the sequence analysis programs blastp, blastn, blastx, tblastn and tblastx. It can be accessed at ~~http://~~www.ncbi.nlm.nih.gov/BLAST. A description of how to determine sequence identity using this program is available at ~~http://~~www.ncbi.nlm.nih.gov/BLAST/blast.help.html.

Please amend the paragraph beginning on Page 17, line 24, as follows:

The alignment tools ALIGN (Myers and Miller, 1989) or LFASTA (pearson and Lipman, 1988) may be used to perform sequence comparisons (Internet Program © 1996, W. R. Pearson and the University of Virginia, "fasta20u63" version 2.0u63, release date December 1996). ALIGN compares entire sequences against one another, while LFAST compares regions of local similarity. These alignment tools and their respective tutorials are available on the internet at ~~http://~~biology.ncsa.uiuc.edu.

Please amend the paragraph beginning on Page 17, line 30, as follows:

In a preferred embodiment, orthologs of the disclosed barley thioredoxin *h* protein are typically characterized by possession of greater than 90.6% sequence identity counted over the full-length alignment with the amino acid sequence of barley thioredoxin *h* using ALIGN set to default parameters. Proteins with even greater similarity to the reference sequences will show increasing percentage identities when assessed by this method, such as at least 92%, at least 93%, at least 95%, at least 96%, at least 97%, at least 98% sequence identity. When less than the entire sequence is being compared for sequence identity, homologs will typically possess at least 90% sequence identity over short window of 10-20 amino acids, and may possess sequence

identities of at least 93%, at least 95%, at least 97%, or at least 99% depending on their similarity to the reference sequence. Sequence identity over such short windows can be determined using LFASTA; methods are described at ~~http://~~biology.ncsa.uiuc.edu. One of skill in the art will appreciate that these sequence identity ranges are provided for guidance only; it is entirely possible that strongly significant homologs could be obtained that fall outside of the ranges provided. The present invention provides not only the peptide homologs that are described above, but also nucleic acid molecules that encode such homologs.